

RAW SEQUENCE LISTING ERROR REPORT



#8

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/004,219
Source: OIPE
Date Processed by STIC: 6-10-02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002

Does Not Comply
Corrected Diskette Needed



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/004,219

DATE: 06/10/2002

TIME: 15:42:24

Input Set: A:\Sequence Listing.txt

Output Set: N:\CRF3\06102002\J004219.raw

3 <110> APPLICANT: Macrozyme
 4 Aerts, Johannes M.F.G.
 5 Boot, Rolf G.
 7 <120> TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
 8 its use in therapy or prophylaxis against diseases in
 9 which mucus is involved or infection diseases
 11 <130> FILE REFERENCE: 2183-5136US
 13 <140> CURRENT APPLICATION NUMBER: 10/004,219
 C--> 14 <141> CURRENT FILING DATE: 2002-06-03
 16 <160> NUMBER OF SEQ ID NOS: 14
 18 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 476
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Artificial Sequence
 W--> 25 <220> FEATURE: ← Whenever numeric identifiers
 25 <223> OTHER INFORMATION: Description of Artificial Sequence: human AMCase
 26 amino acid sequence deduced from cDNA sequence
 E--> 28 <400> SEQUENCE: 1
 29 Met Thr Lys Leu Ile Leu Thr Gly Leu Val Leu Ile Leu Asn Leu
 30 1 5 10 15
 32 Gln Leu Gly Ser Ala Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala
 33 20 25 30
 35 Gln Tyr Arg Pro Gly Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro
 36 35 40 45
 38 Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn
 39 50 55 60
 41 Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe
 42 65 70 75 80
 44 Asn Gly Leu Lys Asn Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile
 45 85 90 95
 47 Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr
 48 100 105 110
 50 Pro Glu Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg
 51 115 120 125
 53 Gln Tyr Glu Phe Asp Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser
 54 130 135 140
 56 Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Gln
 57 145 150 155 160

←
 <221>, <222>, or <223> are used
 numeric identifier <220> is
 mandatory

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Input Set : A:\Sequence Listing.txt
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59 Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro
60 165 170 175
62 Arg Leu Met Val Thr Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln
63 180 185 190
65 Ser Gly Tyr Glu Ile Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His
66 195 200 205
68 Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu
69 210 215 220
71 Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr
72 225 230 235 240
74 Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro
75 245 250 255
77 Ala Glu Lys Leu Ile Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile
78 260 265 270
80 Leu Ser Asn Pro Ser Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala
81 275 280 285
83 Gly Pro Ala Gly Pro Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr
84 290 295 300
86 Glu Ile Cys Thr Phe Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala
87 305 310 315 320
89 Pro Gln Glu Val Pro Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr
90 325 330 335
92 Asp Asn Ile Lys Ser Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn
93 340 345 350
95 Lys Phe Gly Gly Ala Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr
96 355 360 365
98 Gly Thr Phe Cys Asn Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys
99 370 375 380
101 Lys Ala Leu Gly Leu Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro
102 385 390 395 400
104 Ile Glu Pro Ile Thr Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly
105 405 410 415
107 Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val
108 420 425 430
110 Arg Ala Asn Gly Leu Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp
111 435 440 445
113 His Cys Val Asn Gly Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu
114 450 455 460
116 Val Phe Asp Thr Ser Cys Asp Cys Cys Asn Trp Ala
117 465 470 475
412 <210> SEQ ID NO: 4
413 <211> LENGTH: 473
414 <212> TYPE: PRT
415 <213> ORGANISM: Artificial Sequence
W--> 416 <220> FEATURE:
416 <223> OTHER INFORMATION: Description of Artificial Sequence: mouse AMCase
417 amino acid sequence deduced from cDNA sequence
E--> 419 <400> SEQUENCE: 4
420 Met Ala Lys Leu Leu Leu Val Thr Gly Leu Ala Leu Leu Asn Ala

see page 1

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421	1	5	10	15												
423	Gln	Leu	Gly	Ser	Ala	Tyr	Asn	Leu	Ile	Cys	Tyr	Phe	Thr	Asn	Trp	Ala
424					20				25						30	
426	Gln	Tyr	Arg	Pro	Gly	Leu	Gly	Ser	Phe	Lys	Pro	Asp	Asp	Ile	Asn	Pro
427						35			40					45		
429	Cys	Leu	Cys	Thr	His	Leu	Ile	Tyr	Ala	Phe	Ala	Gly	Met	Gln	Asn	Asn
430						50			55			60				
432	Glu	Ile	Thr	Thr	Ile	Glu	Trp	Asn	Asp	Val	Thr	Leu	Tyr	Lys	Ala	Phe
433						65			70			75			80	
435	Asn	Asp	Leu	Lys	Asn	Arg	Asn	Ser	Lys	Leu	Lys	Thr	Leu	Leu	Ala	Ile
436							85			90				95		
438	Gly	Gly	Trp	Asn	Phe	Gly	Thr	Ala	Pro	Phe	Thr	Thr	Met	Val	Ser	Thr
439						100			105			110				
441	Ser	Gln	Asn	Arg	Gln	Thr	Phe	Ile	Thr	Ser	Val	Ile	Lys	Phe	Leu	Arg
442						115			120			125				
444	Gln	Tyr	Gly	Phe	Asp	Gly	Leu	Asp	Leu	Asp	Trp	Glu	Tyr	Pro	Gly	Ser
445						130			135			140				
447	Arg	Gly	Ser	Pro	Pro	Gln	Asp	Lys	His	Leu	Phe	Thr	Val	Leu	Val	Lys
448						145			150			155			160	
450	Glu	Met	Arg	Glu	Ala	Phe	Glu	Gln	Glu	Ala	Ile	Glu	Ser	Asn	Arg	Pro
451							165			170			175			
453	Arg	Leu	Met	Val	Thr	Ala	Ala	Val	Ala	Gly	Gly	Ile	Ser	Asn	Ile	Gln
454						180			185			190				
456	Ala	Gly	Tyr	Glu	Ile	Pro	Glu	Leu	Ser	Lys	Tyr	Leu	Asp	Phe	Ile	His
457						195			200			205				
459	Val	Met	Thr	Tyr	Asp	Leu	His	Gly	Ser	Trp	Glu	Gly	Tyr	Thr	Gly	Glu
460						210			215			220				
462	Asn	Ser	Pro	Leu	Tyr	Lys	Tyr	Pro	Thr	Glu	Thr	Gly	Ser	Asn	Ala	Tyr
463						225			230			235			240	
465	Leu	Asn	Val	Asp	Tyr	Val	Met	Asn	Tyr	Trp	Lys	Asn	Asn	Gly	Ala	Pro
466							245			250			255			
468	Ala	Glu	Lys	Leu	Ile	Val	Gly	Phe	Pro	Glu	Tyr	Gly	His	Thr	Phe	Ile
469						260			265			270				
471	Leu	Arg	Asn	Pro	Ser	Asp	Asn	Gly	Ile	Gly	Ala	Pro	Thr	Ser	Gly	Asp
472						275			280			285				
474	Gly	Pro	Ala	Gly	Ala	Tyr	Thr	Arg	Gln	Ala	Gly	Phe	Trp	Ala	Tyr	Tyr
475						290			295			300				
477	Glu	Ile	Cys	Thr	Phe	Leu	Arg	Ser	Gly	Ala	Thr	Glu	Val	Trp	Asp	Ala
478						305			310			315			320	
480	Ser	Gln	Glu	Val	Pro	Tyr	Ala	Tyr	Lys	Ala	Asn	Glu	Trp	Leu	Gly	Tyr
481							325			330			335			
483	Asp	Asn	Ile	Lys	Ser	Phe	Ser	Val	Lys	Ala	Gln	Trp	Leu	Lys	Gln	Asn
484						340			345			350				
486	Asn	Phe	Gly	Gly	Ala	Met	Ile	Trp	Ala	Ile	Asp	Leu	Asp	Asp	Phe	Thr
487						355			360			365				
489	Gly	Ser	Phe	Cys	Asp	Gln	Gly	Lys	Phe	Pro	Leu	Thr	Ser	Thr	Leu	Asn
490						370			375			380				
492	Lys	Ala	Leu	Gly	Ile	Ser	Thr	Glu	Gly	Cys	Thr	Ala	Pro	Asp	Val	Pro
493						385			390			395			400	

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495 Ser Glu Pro Val Thr Thr Pro Pro Gly Ser Gly Ser Gly Gly Ser
496 405 410 415
498 Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Asp Lys Ala Asp
499 420 425 430
501 Gly Leu Tyr Pro Val Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile
502 435 440 445
504 Asn Gly Ile Thr Tyr Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp
505 450 455 460
507 Thr Ser Cys Asn Cys Asn Trp Pro ..
508 465 470

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/004,219

DATE: 06/10/2002
TIME: 15:42:25

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\06102002\J004219.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:25 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:28 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:1
L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:189 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:416 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:419 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:4